

08/249671

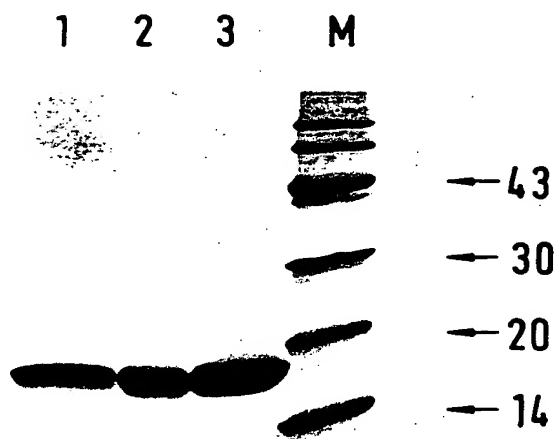
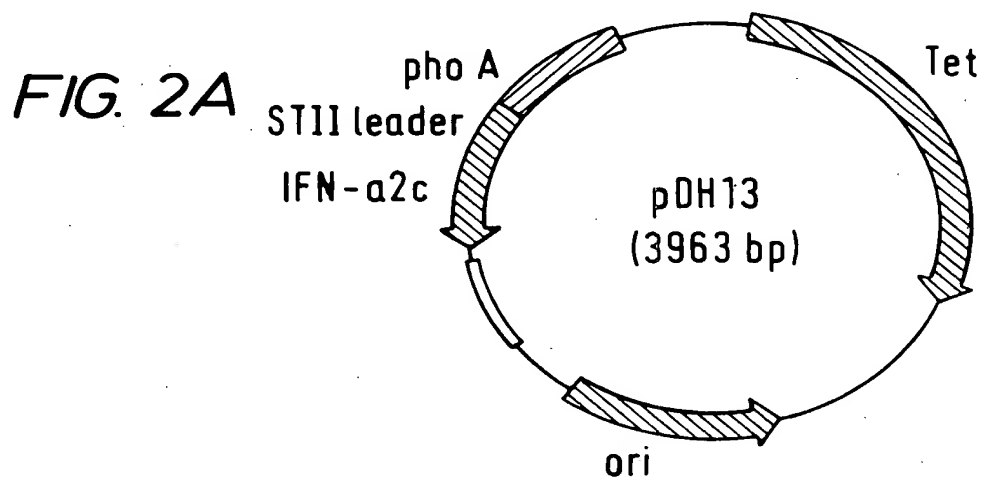
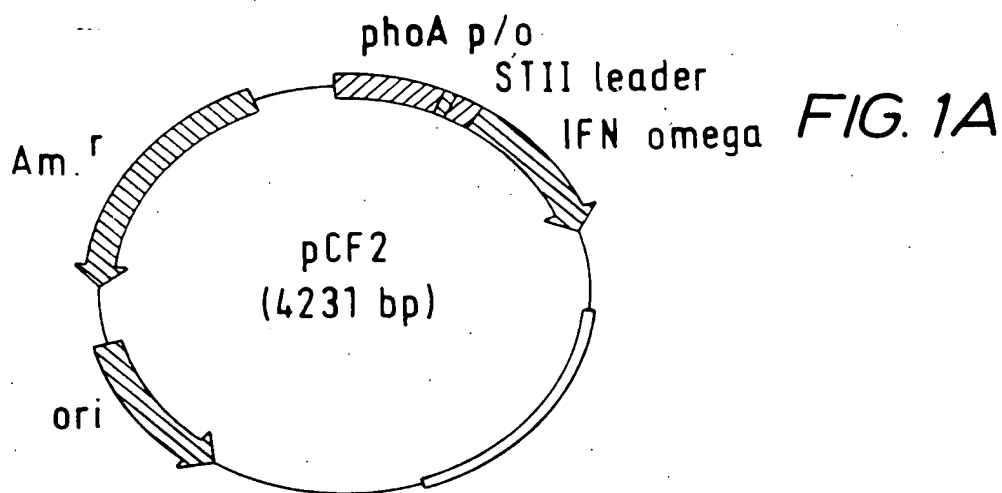


FIG. 4

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FIG. 1B

gaattggagattatcgctcactgcaatgcttcgcaatatggcgcaaaatgaccaac	55
agcggttgattgatacaggtagaggggctgtacgaggtaaagcccgatgccag	110
cattcctgacgacgatacggagctgctgcgcgattacgtaaagaagtattgaag	165
catcctcgtcagtaaaaagttaatacttttcaacagctgtcataaagttgtcacgg	220
ccgagacttatagtcgctttgtttttatttttaattgatttgcctcgagaggttg	275
aggtgatattt ATG AAA AAG AAT ATC GCA TTT CTT CTT GCA TCT	318
M K K N I A F L L A S	11
ATG TTC GTT TTT TCT ATT GCT ACA AAT GCC TAT GCA TGT GAT	360
M F V F S I A T N A Y A C D	25
CTG CCT CAG AAC CAT GGC CTA CTT AGC AGG AAC ACC TTG GTG	402
L P Q N H G L L S R N T L V	39
CTT CTG CAC CAA ATG AGG AGA ATC TCC CCT TTC TTG TGT CTC	444
L L H Q M R I S P F L C L	53
AAG GAC AGA AGA GAC TTC AGG TTC CCC CAG GAG ATG GTA AAA	486
K D R R D F R F P Q E M V K	67
GGG AGC CAG TTG CAG AAG GCC CAT GTC ATG TCT GTC CTC CAT	528
G S Q L Q K A H V M S V L H	81
GAG ATG CTG CAG CAG ATC TTC AGC CTC TTC CAC ACA GAG CGC	570
E M L Q Q I F S L F H T E R	95

FIG. 1B (CONTD)

FIG. 1B (CONTD)

FIG. 2B

ECORI

gaattcgagattatcgctcactgcaatgcttcgcaatatggcgcaaaatgaccaac 55
agcggttgattgatcagtagaggggctgtacgaggtaaagcccgatgccag 110
cattcctgacgacgatacggagctgctgcggttacgtaaaagaattattgaag 165
catcctcgtagtaaaaagttaattcttttcaacagctgtcataaaagtgtcacgg 220

XhoI

ccgagacttatagtcgctttgtttttattttttaatgtatttgcgcgagaggttg 275

STII Leader peptide ->

aggtgatttt ATG AAA AAG AAT ATC GCA TTT CTT CTT GCA TCT 318
M K K N I A F L L A S 11

IFN α 2c ->

ATG TTC GTT TTT TCT ATT GCT ACA AAT GCC TAT GCA TGT GAT 360
M F V F S I A T N A Y A C D 25
CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG ACC TTG ATG 402
L P Q T H S L G S R R T L M 39
CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG 444
L L A Q M R R I S L F S C L 53
AAG GAC AGA CGT GAC TTT GGA TTT CCC CAG GAG TTT GGC 486
K D R R D F G F P Q E E F G 67

AAC CAG TTC CAA AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG	528
N Q F Q K A E T I P V L H E	81
ATG ATC CAG CAG ATC TTC AAT CTC TTC AGC ACA AAG GAC TCA	570
M I Q Q I F N L F S T K D S	95
TCT GCT GCT TGG GAT GAG ACC CTC CTA GAC AAA TTC TAC ACT	612
S A A W D E T L L D K F Y T	109
GAA CTC TAC CAG CAG CTG AAT GAC CTG GAA GCC TGT GTG ATA	654
E L Y Q Q L N D L E A C V I	123
CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG GAG GAC	696
Q G V G V T E T P L M K E D	137
TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC	738
S I L A V R K Y F Q R I T L	151
TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG GAG GTT	780
Y L K E K K Y S P C A W E V	165
GTC AGA GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC	822
V R A E I M R S F S L S T N	179
PvuI PstI	
TTG CAA GAA AGT TTA AGA AGT AAG GAA tgataacgacgtaactgc	868
L Q E S L R S K E	188
HindIII	
agaagctt	876

FIG. 2B(CONTD)

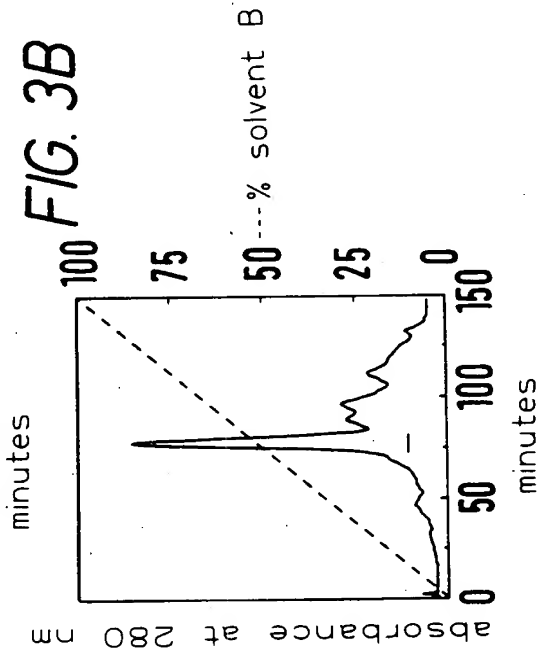
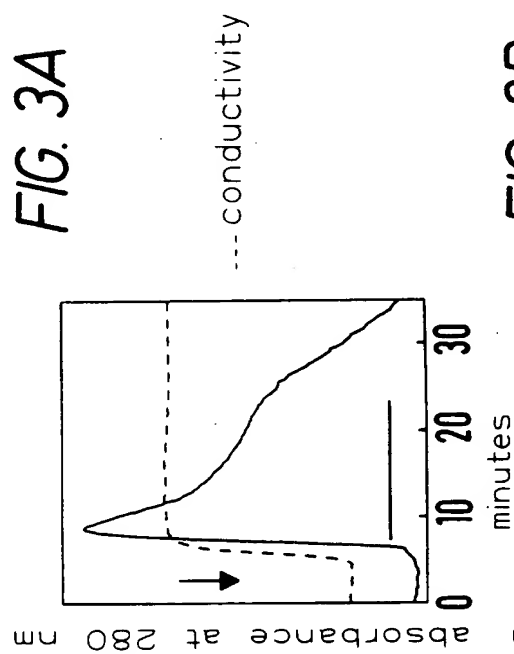
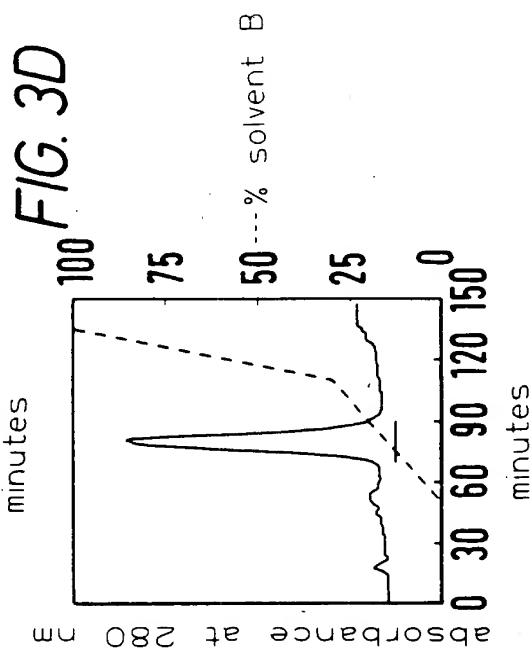
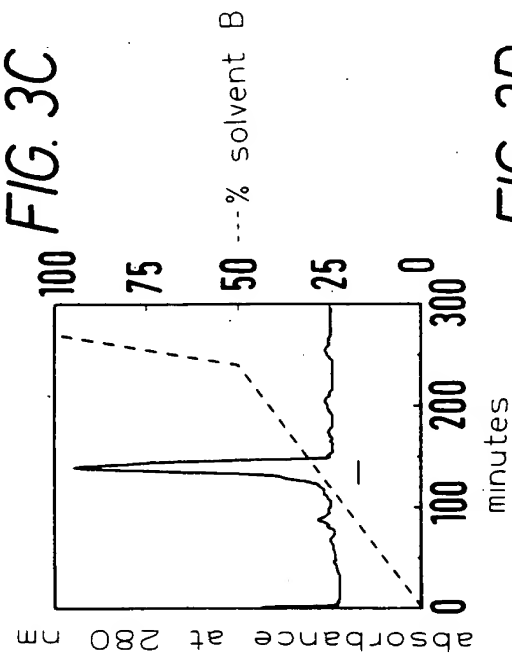


FIG. 5A

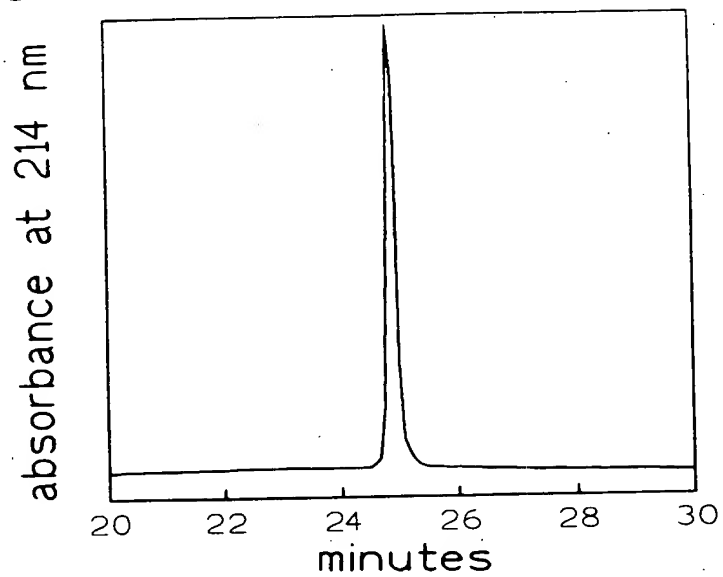
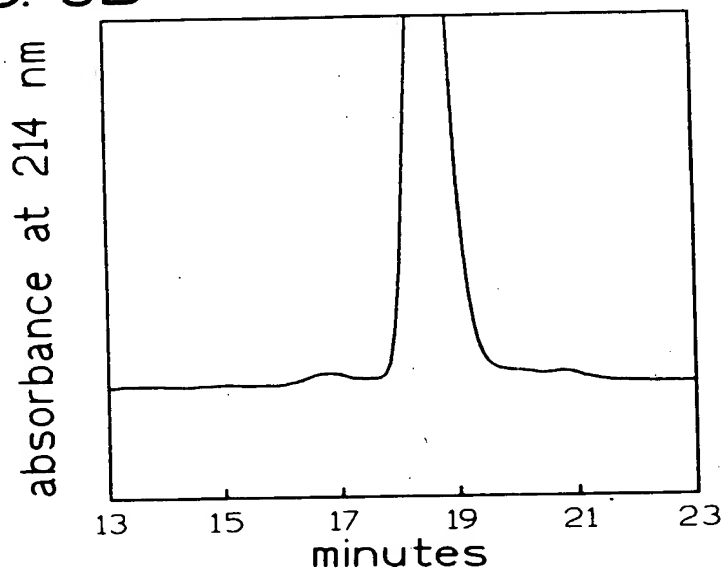


FIG. 5B



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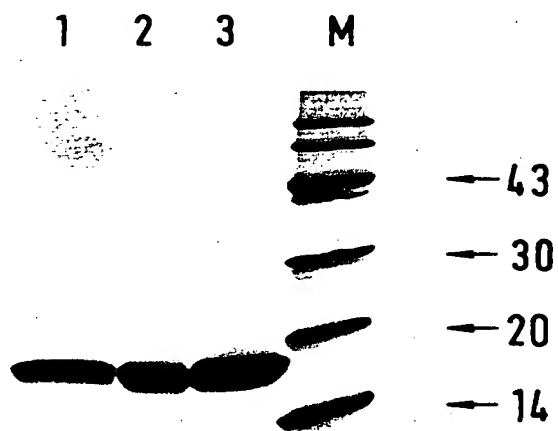
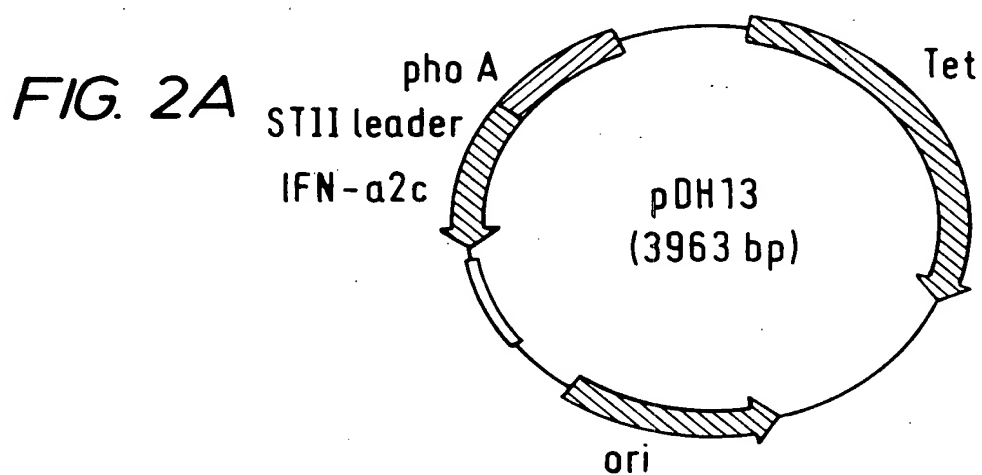
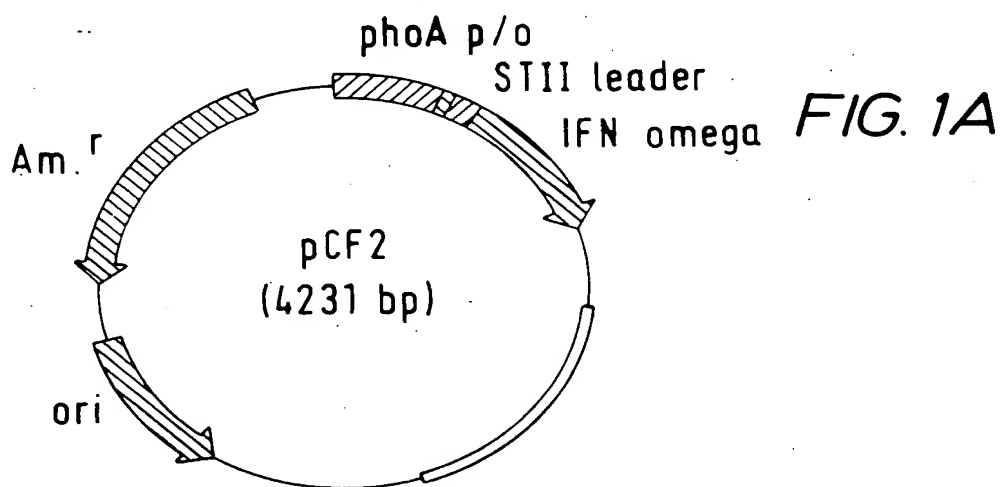


FIG. 4

08/249671

FIG. 1B

gaattggagattatcgctcactgcaatgcttcgcaatatggcgcaaaatgaccaac	55
agcggttgattgattcaggtagaggggctgtacgaggtaaagcccgatgccag	110
cattcctgacgacgatacgagctgctgcgcgattacgtaagaagtattgaag	165
catcctcgtagtaaaaaagttaatcttttcaacagctgtcataaagttgtcacgg	220
ccgagacttatagtcgctttgttttatttttaattgatttgcctcgagaggttg	275
aggtgatattt ATG AAA AAG AAT ATC GCA TTT CTT CTT GCA TCT	318
M K K N I A F L L A S	11
ATG TTC GTT TTT TCT ATT GCT ACA AAT GCC TAT GCA TGT GAT	360
M F V F S I A T N A Y A C D	25
CTG CCT CAG AAC CAT GGC CTA CTT AGC AGG AAC ACC TTG GTG	402
L P Q N H G L L S R N T L V	39
CTT CTG CAC CAA ATG AGG AGA ATC TCC CCT TTC TTG TGT CTC	444
L L H Q M R R I S P F L C L	53
AAG GAC AGA AGA GAC TTC AGG TTC CCC CAG GAG ATG GTA AAA	486
K D R R D F R F P Q E M V K	67
GGG AGC CAG TTG CAG AAG GCC CAT GTC ATG TCT GTC CTC CAT	528
G S Q L Q K A H V M S V L H	81
GAG ATG CTG CAG CAG ATC TTC AGC CTC TTC CAC ACA GAG CGC	570
E M L Q Q I F S L F H T E R	95

FIG. 1B (CONTD)

FIG. 2B

ECORI

gaattcgagattatcgtcactgcaatgcttcgcaatatggcgcaaaatgaccaac 55
agcggttgattgatcaggtagagggggtgctgtacgaggtaaagcccgatgccag 110
cattcctgacgacgatacggagctgctgctgacgattacgtaaaagaattattgaag 165
catcctcgtaaaaaagtttaattcttttcaacagctgtcataaagttgtcacgg 220

XhoI

ccgagacttatagtcgcttggttttttatttttttaattgttctcgagaggttg 275

STII Leader peptide ->

aggtgatttt ATG AAA AAG AAT ATC GCA TTT CTT CTT GCA TCT 318
M K K N I A F L L A S 11

IFNa2c ->

ATG TTC GTT TTT TCT ATT GCT ACA AAT GCC TAT GCA TGT GAT 360
M F V F S I A T N A Y A C D 25
CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG ACC TTG ATG 402
L P Q T H S L G S R R T L M 39
CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG 444
L L A Q M R R I S L F S C L 53
AAG GAC AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC 486
K D R R D F G G F P O E E F G 67

AAC CAG TTC CAA AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG	528
N Q F Q K A E T I P V L H E	81
ATG ATC CAG CAG ATC TTC AAT CTC TTC AGC ACA AAG GAC TCA	570
M I Q Q I F N L F S T K D S	95
TCT GCT GCT TGG GAT GAG ACC CTC CTA GAC AAA TTC TAC ACT	612
S A A W D E T L L D K F Y T	109
GAA CTC TAC CAG CAG CTG AAT GAC CTG GAA GCC TGT GTG ATA	654
E L Y Q Q L N D L E A C V I	123
CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG GAG GAC	696
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TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC	738
S I L A V R K Y F Q R I T L	151
TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG GAG GTT	780
Y L K E K K Y S P C A W E V	165
GTC AGA GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC	822
V R A E I M R S F S L S T N	179
	PvuI PstI
TTG CAA GAA AGT TTA AGA AGT AAG GAA tgataacgacgtaactgc	868
L Q E S L R S K E	188
HindIII	
agaagctt	876

FIG. 2B (CONT'D)

